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1: Mol Phylogenet Evol 1999 Oct;13(1):82-92

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FULL-TEXT ARTICLE

Rapid radiation events in the family Ursidae indicated by likelihood phylogenetic estimation from multiple fragments of mtDNA.

Waits LP, Sullivan J, O'Brien SJ, Ward RH.

Department of Fish and Wildlife Resources, University of Idaho, Moscow 83844-1136, USA.

The bear family (Ursidae) presents a number of phylogenetic ambiguities as the evolutionary relationships of the six youngest members (ursine bears) are largely unresolved. Recent mitochondrial DNA analyses have produced conflicting results with respect to the phylogeny of ursine bears. In an attempt to resolve these issues, we obtained 1916 nucleotides of mitochondrial DNA sequence data from six gene segments for all eight bear species and conducted maximum likelihood and maximum parsimony analyses on all fragments separately and combined. All six single-region gene trees gave different phylogenetic estimates; however, only for control region data was this significantly incongruent with the results from the combined data. The optimal phylogeny for the combined data set suggests that the giant panda is most basal followed by the spectacled bear. The sloth bear is the basal ursine bear, and there is weak support for a sister taxon relationship of the American and Asiatic black bears. The sun bear is sister taxon to the youngest clade containing brown bears and polar bears. Statistical analyses of alternate hypotheses revealed a lack of strong support for many of the relationships. We suggest that the difficulties surrounding the resolution of the evolutionary relationships of the Ursidae are linked to the existence of sequential rapid radiation events in bear evolution. Thus, unresolved branching orders during these time periods may represent an accurate representation of the evolutionary history of bear species. Copyright

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